

Abstract Submitted  
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**Frustration in Condensed Matter and Protein Folding**<sup>1</sup> S  
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of computer modeling, we are studying frustration in condensed matter and pro-  
tein folding. Frustration is due to random and/or competing interactions between  
characters. One definition of frustration is the sum of squares of the differences  
between actual and expected distances between characters. If this sum is non-zero  
then the system is said to have frustration. A computer simulation “Frustration” is  
used to track the movement of characters to lower their frustration. Our research is  
conducted on frustration as a function of temperature using a logarithmic scale. At  
absolute zero, the relaxation for frustration is mostly a power function for randomly  
assigned patterns or an exponential function for regular patterns like Thomson fig-  
ures. Thomson shapes are formed and the temperature-dependent frustration shows  
exponential behavior. At later times a linear trend sets in, close to zero or finite frus-  
tration. These findings have implications for protein folding; we attempt to apply  
our frustration modeling to protein folding and dynamics. We use coding in Python  
to simulate different ways a protein can fold. An algorithm is being developed to  
find the lowest frustration (and thus energy) states possible.

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